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A Single Nucleotide Replacement Restores Methamphetamine Traits to Low Addiction Risk Levels

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A spontaneous mutation arose in the trace amine-associated receptor 1 gene, *Taar1*, in DBA/2J (D2) mice at The Jackson Laboratory in 2001-2003. Homozygosity for the mutant allele (*Taar1*^{m1J}) corresponds with high methamphetamine (MA) intake on multiple genetic backgrounds, including pure D2, mixed C57BL/6J x D2 and heterogeneous stock collaborative cross x D2. Low sensitivity to aversive effects of MA corresponds with high MA intake and also appears to be impacted by this mutation. MA is a direct agonist at TAAR1 and this mutation eliminates receptor function. We hypothesized that restored function would reverse these high MA addiction risk phenotypes. To examine this, the native *Taar1*⁺ allele was inserted into the genome of mice bred for high MA intake, which are homozygous for the *Taar1*^{m1J} allele. CRISPR-Cas9 was used to first excise the *Taar1*^{m1J} variant and then replace it with the *Taar1*⁺ variant, thus restoring TAAR1 function. These mice were compared to non-altered controls for 3 MA phenotypes. All phenotypes were restored to levels found in mice with the *Taar1*⁺ allele that codes for a functional protein. Thus, MA intake was low and sensitivity to aversive and hypothermic effects of MA was high, compared to controls. These results confirm a causal role for *Taar1* in MA intake, and suggest that functional TAAR1 maintains sensitivity to effects of MA that may protect from excessive use. Some human TAAR1 variants have been identified that impact TAAR1 function and may alter sensitivity to effects of MA that are relevant to risk for MA use.